

Figure 1: 108P5H8 SSH sequence of 448 nucleotides (SEQ ID: 2568)

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1 GATCCAGATT TCTCTGCACA CTGGACTTCG TAGAGTAAGT GTGGTAGACA AAGAGACTAC
61 ACTGCACAAC CACCAGTGAA TATCATTGCT AAGAAGACTT TGGGTCGTGT TTCTCAGCCA
121 CTCTCACAGC TTTTGTAGAC TTATTTGATT TTGAAACAAG CAGTTAGCTA AATCTATTTT
181 CCTTTTATGC ATATATGTTA ATTGGCTCAA CTTAATATGG TGTTCTTACA GAATATGAGC
241 CCATTTGAAA TAAGGTTTTA GGCAATTTTG CTGTTGGCTC TGATTTGTAT ATAGCAAATT
301 TAAAGGTACA GAGTGTTC TAGATAGAAG ATTAGTTCAT TTGGTTCATT TTGTCTTTGA
361 AGCAAGCCAA GTCATGAGC CAGTTGGTTA TTTGTCATAA ATGAACACCC ATCACTATAT
421 GCTATGTTGA GGGGAGGCAA GGCTGATC
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Figure 2A. The cDNA (SEQ ID. NO. :2569) and amino acid sequence (SEQ ID. NO. :2570) of 108P5H8 v.1. The start methionine is underlined. The open reading frame extends from nucleic acid 253-1542 including the stop codon.

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1 gccggcctccagcagcgggcgcgggcgcgagcacgacccactctcctgcggccgcg
61 ggtggagcagcgcgagccgcctcgctgagccggccggggcggggagatgagttgcggc
121 cccgcggcagcgcgccagcatggggagggacgcgcggcactgccctcgagaactggcgct
181 ccggtgaagtaggcgccgcggccgctccgcctcccccagccggttcgcacccgcggccgc
1 M A G S G A W K R L K S M L R K
241 tcagecctctgccATGGCCGGCTCTGGCGCGTGGAAGCGCCTCAAATCTATGCTAAGGAAG
17 D D A P L F L N D T S A F D F S D E A G
301 GATGATGCGCCGCTGTTTTTAAATGACACCAGCGCCTTTGACTTCTCGGATGAGGCGGG
37 D E G L S R F N K L R V V V A D D G S E
361 GACGAGGGGCTTTCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAA
57 A P E R P V N G A H P T L Q A D D D S L
421 GCCCCGAAAGGCCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCCTTA
77 L D Q D L P L T N S Q L S L K V D S C D
481 CTGGACCAAGACTTACCITTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGAC
97 N C S K Q R E I L K Q R K V K A R L T I
541 AACTGCAGCAAACAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATT
117 A A V L Y L L F M I G E L V G G Y I A N
601 GCTGCCGTTCTGTACTTGCTTTTCATGATTGGAGAACTTGTAGGTGGATACATTGCAAAT
137 S L A I M T D A L H M L T D L S A I I L
661 AGCCTAGCAATCATGACAGATGCACITTCATATGTAACTGACCTAAGCGCCATCATACTC
157 T L L A L W L S S K S P T K R F T F G F
721 ACCCTGCTTGCTTTGTGGCTATCATAAAATCACCAACCAAAAGATTACCTTTGGATTT
177 H R L E V L S A M I S V L L V Y I L M G
781 CATCGCTTAGAGGTTTTGTCTAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGA
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197 F L L Y E A V Q R T I H M N Y E I N G D
841 TTCCTCTTATATGAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGAT
217 I M L I T A A V G V A V N V I M G F L L
901 ATAATGCTCATCACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTG
237 N Q S G H R H S H S H S L P S N S P T R
961 AACCAGTCTGGTCACCGTCACTCCCATTCCCCTCCCTGCCTTCAAATTCCCCCTACCAGA
257 G S G C E R N H G Q D S L A V R A A F V
1021 GGTTCCTGGGTGTGAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTGTGA
277 H A L G D L V Q S V G V L I A A Y I I R
1081 CATGCTTTGGGAGATTTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGA
297 F K P E Y K I A D P I C T Y V F S L L V
1141 TTCAAGCCAGAATACAAGATTGCTGACCCCATCTGTACATACGTATTTTCATTACTTGTG
317 A F T T F R I I W D T V V I I L E G V P
1201 GCTTTTACAACATTTTGAATCATATGGGATACAGTAGTTATAATACTAGAAAGGTGTGCCA
337 S H L N V D Y I K E A L M K I E D V Y S
1261 AGCCATTTGAATGTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCA
357 V E D L N I W S L T S G K S T A I V H I
1321 GTCGAAGATTTAAATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATA
377 Q L I P G S S S K W E E V Q S K A N H L
1381 CAGCTAATTCCTGGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTTA
397 L L N T F G M Y R C T I Q L Q S Y R Q E
1441 TTATTGAACACATTTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAA
417 V D R T C A N C Q S S S P *
1501 GTGGACAGAACTTGTGCAAATTGTGAGAGTCTAGTCCCTAAAttttatgtattttgggaa
1561 ctctctgccttattttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatga
1621 gaaaatggaatccctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccc
1681 cagcctgacagtgctagtctctgtttaatggtaaaaggagactttgccataattttcaga
1741 tgaagatgtttcccaaactgtttacagaatgagatgtgactctacagatacctcatag
1801 aagacaatccaagatcatacttcattaacttgacagagtacgtgtcttaaagggaagcatc
1861 aagaattcaatattttgcatttaaaaaatactttttaaggccattttatattaagccagtg
1921 tggaaaactgaattttttttattatgtataataatctcgacaccagcttctggaattgc
1981 tgctttctttttacagaaattactacccaacagatttcaggaagtactagtagttatccc
2041 aaaagtggaaataagcatgtattcctaagtgtttcagaaatgttttatttcacacataagt
2101 cttaatgttattgttatgattatactttataaacaaccttttccagatgctacagggttt
2161 tgaatctcaaagttaacattttttcattatttgtaatcttagaaccaaatctttattttatt
2221 gtggtcactgttattaaatgatttaggaaatactttcaatattattctgaatggctgaag
2281 ttagtcttaaaactcaaattactatatgatgattttaaaacaaaataaaagagcgaggatgg
2341 ggaaaaaaaaaaaaaaaaaaaaa

Figure 2B. The cDNA (SEQ ID. NO. :2571) and amino acid sequence (SEQ ID. NO. :2572) of 108P5H8 v.2. The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.

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1 M A G S G A W K R L K S M L R K D D A P
1 ATGGCCGGCTCTGGCGCTGGAAGCGCCTCAAATCTATGCTAAGGAAGGATGATGCGCCG
21 L F L N D T S A F D F S D E A G D E G L
61 CTGTTTTTTAAATGACACCAGCGCCTTTGACTTCTCGGATGAGGCGGGGACGAGGGGCTT
41 S R F N K L R V V V A D D G S E A P E R
121 TCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAAGCCCCGAAAGG
61 P V N G A H P T L Q A D D D S L L D Q D
181 CCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCTTACTGGACCAAGAC
81 L P L T N S Q L S L K V D S C D N C S K
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGACAACGACAGCAA
101 Q R E I L K Q R K V K A R L T I A A V L
301 CAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATTGCTGCCGTTCTG
121 Y L L F M I G E L V G G Y I A N S L A I
361 TACTTGCTTTTCATGATTGGAGAAGTTGTAGGTGGATACATTGCAAATAGCCTAGCAATC
141 M T D A L H M L T D L S A I I L T L L A
421 ATGACAGATGCACTTCATATGTAACTGACCTAAGCGCCATCATACTCACCTGCTTGCT
161 L W L S S K S P T K R F T F G F H R L E
481 TTGTGGCTATCATCAAAATCACCAACCAAAAGATTACCTTTGGATTTTCATCGCTTAGAG
181 V L S A M I S V L L V Y I L M G F L L Y
541 GTTTTGTGAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGATTCCTCTTATAT
201 E A V Q R T I H M N Y E I N G D I M L I
601 GAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGATATAATGCTCATC
221 T A A V G V A V N V I M G F L L N Q S G
661 ACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACCAGTCTGGT
241 H R H S H S H S L P S N S P T R G S G C
721 CACCGTCACTCCCATTCCCCTCCCTGCCTTCAAATCCCCTACCAGAGGTTCTGGGTGT
261 E R N H G Q D S L A V R A A F V H A L G
781 GAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTTGTACATGCTTTGGGA
281 D L V Q S V G V L I A A Y I I R F K P E
841 GATTTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGATTCAAGCCAGAA
301 Y K I A D P I C T Y V F S L L V A F T T
901 TACAAGATTGCTGATCCCATCTGTACATACGTATTTTCATTACTTGTGGCTTTTACAACA
321 F R I I W D T V V I I L E G V P S H L N
961 TTTCGAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCAAGCCATTTGAAT
341 V D Y I K E A L M K I E D V Y S V E D L
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1021 GTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCAGTCGAAGATTTA
361 N I W S L T S G K S T A I V H I Q L I P
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT
381 G S S S K W E E V Q S K A N H L L L N T
1141 GGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTTATTATTGAACACA
401 F G M Y R C T I Q L Q S Y R Q E V D R T
1201 TTTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAAGTGGACAGAACT
421 C A N C Q S S S P *
1261 TGTGCAAATTGTCAGAGTTCTAGTCCCTAAAttttatgtattttggggactcctgccttat
1321 ttatcctgcagtcacagacttgagagcaataaatgcaaaccctaaatgagaaaatggaatc
1381 cctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccccagcctgacagt
1441 gctagtctctgtttaatggtaaaaggagactttgccataattttcagatgaagatgtttc
1501 ccaaacactgtttacagaatgagatgtgactctacagatacctcatag

Figure 2C. The cDNA (SEQ ID. NO. :2573) and amino acid sequence (SEQ ID. NO. :2574) of 108P5H8 v.3. The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.

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1 M A G S G A W K R L K S M L R K D D A P
1 ATGGCCGGCTCTGGCGCGTGGAAGCGCCTCAAATCTATGCTAAGGAAGGATGATGCGCCG
21 L F L N D T S A F E F S D E A G D E G L
61 CTGTTTTTAAATGACACCAGCGCCTTTGAGTTCTCGGATGAGGCGGGGACGAGGGGCTT
41 S R F N K L R V V V A D D G S E A P E R
121 TCTCGGTTCAACAAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAAGCCCCGAAAGG
61 P V N G A H P T L Q A D D D S L L D Q D
181 CCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCTTACTGGACCAAGAC
81 L P L T N S Q L S L K V D S C D N C S K
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGACAACTGCAGCAAA
101 Q R E I L K Q R K V K A R L T I A A V L
301 CAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATTGCTGCCGTTCTG
121 Y L L F M I G E L V G G Y I A N S L A I
361 TACTTGCTTTTCATGATTGGAGAACTTGTAGGTGGATACATTGCAAATAGCCTAGCAATC
141 M T D A L H M L T D L S A I I L T L L A
421 ATGACAGATGCACTTCATATGTAACTGACCTAAGCGCCATCATACTCACCCCTGCTTGCT
161 L W L S S K S P T K R F T F G F H R L E
481 TTGTGGCTATCATCAAAATCACCAACCAAAAGATTACCTTTGGATTTCATCGCTTAGAG
181 V L S A M I S V L L V Y I L M G F L L Y
541 GTTTTGTACAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGATTCCTCTTATAT
201 E A V Q R T I H M N Y E I N G D I M L I
601 GAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGATATAATGCTCATC
221 T A A V G V A V N V I M G F L L N Q S G
661 ACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACCAGTCTGGT
241 H R H S H S H S L P S N S P T R G S G C
721 CACCGTCACTCCCATTCCCCTCCCTGCCTTCAAATTCCCCTACCAGAGGTTCTGGGTGT
261 E R N H G Q D S L A V R A A F V H A L G
781 GAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTTGTACATGCTTTGGGA
281 D L V Q S V G V L I A A Y I I R F K P E
841 GATCTGGTACAGAGTGTTGGTGTGCTAATAGCTGCATACATCATACGATTCAAGCCAGAA
301 Y K I A D P I C T Y V F S L L V A F T T
901 TACAAGATTGCTGACCCCATCTGTACATACGTATTTTCATTACTTGTGGCTTTTACAACA
321 F R I I W D T V V I I L E G V P S H L N
961 TTTCGAATCATATGGGATACAGTAGTTATAATACTAGAAAGGTGTGCCAAGCCATTTGAAT
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341 V D Y I K E A L M K I E D V Y S V E D L
1021 GTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCAGTCGAAGATTTA
361 N I W S L T S G K S T A I V H I Q L I P
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT
381 G S S S K W E E V Q S K A N H L L L N T
1141 GGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTTATTATTGAACACA
401 F G M Y R C T I Q L Q S Y R Q E V D R T
1201 TTTGGCATGTATAGATGTACTATTCAGCTTCAGAGTTACAGGCAAGAAGTGGACAGAACT
421 C A N C Q S S S P *
1261 TGTGCAAATTGTCAGAGTTCTAGTCCCTAAttttatgtattgttttagcattgctgaatt
1321 cactttatttatcctgcagtcacagacttgagagcaataaatgcaaaccctaaatgagaaa
1381 atggaatccctgacagctgtgtccgtatcaagcatcagttctctcaaacagttgccccagc
1441 ctgacagtgctagtctctgtttaatggtaaaaggagactttgccataattttcagatgaa
1501 gatgtttcccaaactgtttacagaatgagatgtgactcctacagatacctcatag

Figure 4:

Figure 4A Nucleic acid sequence alignment of the 3 variants of 108P5H8. (SEQ ID NOs: 2569, 2571 & 2573). Highlighted in yellow and underlined are the variations between the variants. The ORF extends from nucleotides 253-1542 of 108P5H8 v.1.

1	15	16	30	31	45	46	60	61	75	76	90
v.1	GCCGGCCCTC	CAGCAG	CGGGCGCGCGGGCGG	CGAGCACGACCCAC	TCTCCTGCGGCGCGG	GGTGAGCAGCGCGA	CCCCGCTCGCTGAG				
v.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
91	105	106	120	121	135	136	150	151	165	166	180
v.1	CCGGCCGGGGCGGG	GAGATGAGTTGCGGC	CCCGCGCAGCGGCC	CAGGATGGGGAGGGA	CGCGGGCACTGCCC	TCGAGAACTGGCGCT					
v.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
181	195	196	210	211	225	226	240	241	255	256	270
v.1	CCGGTGAAGTAGGCG	CGCGCGGCGGTCGCG	CTCCCCCAAGCGGT	CGCACCGCGGCGCG	TCAGCCTCTGCCATG	GCCGGCTCTGGCGCG					
v.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
271	285	286	300	301	315	316	330	331	345	346	360
v.1	TGGAAGCGGCTCAAA	ICTATGCTAAGGAAG	GATGATGCGCGGCTG	TTTTTAAATGACACC	AGCGCCTTTGAC	TTTC	TCGGATGAGGCGGGG				
v.2	TGGAAGCGGCTCAAA	ICTATGCTAAGGAAG	GATGATGCGCGGCTG	TTTTTAAATGACACC	AGCGCCTTTGAC	TTTC	TCGGATGAGGCGGGG				
v.3	TGGAAGCGGCTCAAA	ICTATGCTAAGGAAG	GATGATGCGCGGCTG	TTTTTAAATGACACC	AGCGCCTTTGAG	TTTC	TCGGATGAGGCGGGG				
361	375	376	390	391	405	406	420	421	435	436	450
v.1	GACGAGGGGCTTTCT	CGGTTCAACAAACTT	CGAGTTGTTGGTGGCC	GATGACGGTTCCGAA	GCCCCGGAAGGCCCT	GTTAACGGGGCGGCAC					
v.2	GACGAGGGGCTTTCT	CGGTTCAACAAACTT	CGAGTTGTTGGTGGCC	GATGACGGTTCCGAA	GCCCCGGAAGGCCCT	GTTAACGGGGCGGCAC					
v.3	GACGAGGGGCTTTCT	CGGTTCAACAAACTT	CGAGTTGTTGGTGGCC	GATGACGGTTCCGAA	GCCCCGGAAGGCCCT	GTTAACGGGGCGGCAC					
451	465	466	480	481	495	496	510	511	525	526	540
v.1	CCGACCCCTCCAGGCC	GACGATGATTCCTTA	CTGGACCAAGACTTA	CCTTTGACCAACAGT	CAGCTGAGTTTGAAG	GTGGACTCCTGTGAC					
v.2	CCGACCCCTCCAGGCC	GACGATGATTCCTTA	CTGGACCAAGACTTA	CCTTTGACCAACAGT	CAGCTGAGTTTGAAG	GTGGACTCCTGTGAC					
v.3	CCGACCCCTCCAGGCC	GACGATGATTCCTTA	CTGGACCAAGACTTA	CCTTTGACCAACAGT	CAGCTGAGTTTGAAG	GTGGACTCCTGTGAC					

541	555	556	570	571	585	586	600	601	615	616	630
v.1	AACTGCAGCAACAG	AGAGAGATACTGAAG	CAGAGAAAGGTGAAA	GCCAGGTTGACCAATT	GCTGCCGTTCTGTAC	TTGCTTTTCAATGATT					
v.2	AACTGCAGCAACAG	AGAGAGATACTGAAG	CAGAGAAAGGTGAAA	GCCAGGTTGACCAATT	GCTGCCGTTCTGTAC	TTGCTTTTCAATGATT					
v.3	AACTGCAGCAACAG	AGAGAGATACTGAAG	CAGAGAAAGGTGAAA	GCCAGGTTGACCAATT	GCTGCCGTTCTGTAC	TTGCTTTTCAATGATT					
631	645	646	660	661	675	676	690	691	705	706	720
v.1	GGAGAACTTGTAGGT	GGATACATTGCAAAAT	AGCCTAGCAATCATG	ACAGATGCACCTTCAT	ATGTTAACTGACCTA	AGCGCCATCATACTC					
v.2	GGAGAACTTGTAGGT	GGATACATTGCAAAAT	AGCCTAGCAATCATG	ACAGATGCACCTTCAT	ATGTTAACTGACCTA	AGCGCCATCATACTC					
v.3	GGAGAACTTGTAGGT	GGATACATTGCAAAAT	AGCCTAGCAATCATG	ACAGATGCACCTTCAT	ATGTTAACTGACCTA	AGCGCCATCATACTC					
721	735	736	750	751	765	766	780	781	795	796	810
v.1	ACCCTGCTTGCTTTG	TGGCTATCATCAAAA	TCACCAACCAAAAAGA	TTCACTTTTGGATTT	CATCGCTTAGAGGTT	TTGTCAGCTATGATT					
v.2	ACCCTGCTTGCTTTG	TGGCTATCATCAAAA	TCACCAACCAAAAAGA	TTCACTTTTGGATTT	CATCGCTTAGAGGTT	TTGTCAGCTATGATT					
v.3	ACCCTGCTTGCTTTG	TGGCTATCATCAAAA	TCACCAACCAAAAAGA	TTCACTTTTGGATTT	CATCGCTTAGAGGTT	TTGTCAGCTATGATT					
811	825	826	840	841	855	856	870	871	885	886	900
v.1	AGTGTGCTGTTGGTG	TATATACTTATGGGA	TTCTCTTTATATGAA	GCTGTGCAAAAGAACT	ATCCATATGAACTAT	GAATAAATGGAGAT					
v.2	AGTGTGCTGTTGGTG	TATATACTTATGGGA	TTCTCTTTATATGAA	GCTGTGCAAAAGAACT	ATCCATATGAACTAT	GAATAAATGGAGAT					
v.3	AGTGTGCTGTTGGTG	TATATACTTATGGGA	TTCTCTTTATATGAA	GCTGTGCAAAAGAACT	ATCCATATGAACTAT	GAATAAATGGAGAT					
901	915	916	930	931	945	946	960	961	975	976	990
v.1	ATAATGCTCATCACC	GCAGCTGTTGGAGTT	GCAGTTAAIGTAATA	ATGGGGTTTCTGTTG	AACCACTCTGGTCAC	CGTCACCTCCCATTC					
v.2	ATAATGCTCATCACC	GCAGCTGTTGGAGTT	GCAGTTAAIGTAATA	ATGGGGTTTCTGTTG	AACCACTCTGGTCAC	CGTCACCTCCCATTC					
v.3	ATAATGCTCATCACC	GCAGCTGTTGGAGTT	GCAGTTAAIGTAATA	ATGGGGTTTCTGTTG	AACCACTCTGGTCAC	CGTCACCTCCCATTC					
991	1005	1006	1020	1021	1035	1036	1050	1051	1065	1066	1080
v.1	CACCTCCCTGCCTTCA	AATCCCTTACCAGA	GGTCTGGGTGTGAA	CGTAACCATGGGCAG	GATAGCCTGGCAGTG	AGAGCTGCATTGTA					
v.2	CACCTCCCTGCCTTCA	AATCCCTTACCAGA	GGTCTGGGTGTGAA	CGTAACCATGGGCAG	GATAGCCTGGCAGTG	AGAGCTGCATTGTA					
v.3	CACCTCCCTGCCTTCA	AATCCCTTACCAGA	GGTCTGGGTGTGAA	CGTAACCATGGGCAG	GATAGCCTGGCAGTG	AGAGCTGCATTGTA					
1081	1095	1096	1110	1111	1125	1126	1140	1141	1155	1156	1170
v.1	CATGCTTTGGGAGAT	TTGGTACAGAGTGT	GGTGTGCTAATAGCT	GCATACATCATACGA	TTCAAGCCAGAATAC	AAGATTGCTGATCCCC					
v.2	CATGCTTTGGGAGAT	TTGGTACAGAGTGT	GGTGTGCTAATAGCT	GCATACATCATACGA	TTCAAGCCAGAATAC	AAGATTGCTGATCCCC					
v.3	CATGCTTTGGGAGAT	TTGGTACAGAGTGT	GGTGTGCTAATAGCT	GCATACATCATACGA	TTCAAGCCAGAATAC	AAGATTGCTGATCCCC					
1171	1185	1186	1200	1201	1215	1216	1230	1231	1245	1246	1260

v.1	ATCTGTACATACGTA	TTTTTCATTACTTGTG	GCTTTTACAACATTT	CGAATCATATGGGAT	ACAGTAGTTATAATA	CTAGAAGGTGTGCCA					
v.2	ATCTGTACATACGTA	TTTTTCATTACTTGTG	GCTTTTACAACATTT	CGAATCATATGGGAT	ACAGTAGTTATAATA	CTAGAAGGTGTGCCA					
v.3	ATCTGTACATACGTA	TTTTTCATTACTTGTG	GCTTTTACAACATTT	CGAATCATATGGGAT	ACAGTAGTTATAATA	CTAGAAGGTGTGCCA					
1261	1275	1276	1290	1291	1305	1306	1320	1321	1335	1336	1350
v.1	AGCCATTTGAATGTA	GACTATATCAAAGAA	GCCTTGATGAAAATA	GAAGATGTATATTCA	GTGGAAGATTTAAAT	ATCTGGTCTCTCAGT					
v.2	AGCCATTTGAATGTA	GACTATATCAAAGAA	GCCTTGATGAAAATA	GAAGATGTATATTCA	GTGGAAGATTTAAAT	ATCTGGTCTCTCAGT					
v.3	AGCCATTTGAATGTA	GACTATATCAAAGAA	GCCTTGATGAAAATA	GAAGATGTATATTCA	GTGGAAGATTTAAAT	ATCTGGTCTCTCAGT					
1351	1365	1366	1380	1381	1395	1396	1410	1411	1425	1426	1440
v.1	TCAGGAAAATCTACT	GCCATAGITTCACATA	CAGCTAATTCCTGGA	AGTTCAATCTAAATGG	GAGGAAGTACAGTCC	AAAGCAAACCATTTA					
v.2	TCAGGAAAATCTACT	GCCATAGITTCACATA	CAGCTAATTCCTGGA	AGTTCAATCTAAATGG	GAGGAAGTACAGTCC	AAAGCAAACCATTTA					
v.3	TCAGGAAAATCTACT	GCCATAGITTCACATA	CAGCTAATTCCTGGA	AGTTCAATCTAAATGG	GAGGAAGTACAGTCC	AAAGCAAACCATTTA					
1441	1455	1456	1470	1471	1485	1486	1500	1501	1515	1516	1530
v.1	TTATTGAACACATTT	GGCATGTATAGATGT	ACTATTCAAGCTTCAG	AGTTACAGGCAAGAA	GTGGACAGAATTTGT	GCAAATTTGTACAGAT					
v.2	TTATTGAACACATTT	GGCATGTATAGATGT	ACTATTCAAGCTTCAG	AGTTACAGGCAAGAA	GTGGACAGAATTTGT	GCAAATTTGTACAGAT					
v.3	TTATTGAACACATTT	GGCATGTATAGATGT	ACTATTCAAGCTTCAG	AGTTACAGGCAAGAA	GTGGACAGAATTTGT	GCAAATTTGTACAGAT					
1531	1545	1546	1560	1561	1575	1576	1590	1591	1605	1606	1620
v.1	TCTAGTCCCTAAATTT	TATGTATT--TTGGG	AACCTCCTG-----C	CTTATTTATCCTGCA	GTCCACAGACTTGAGA	GCAATAAATGCAAAAC					
v.2	TCTAGTCCCTAAATTT	TATGTATT--TTGGG	GACTCCTG-----C	CTTATTTATCCTGCA	GTCCACAGACTTGAGA	GCAATAAATGCAAAAC					
v.3	TCTAGTCCCTAAATTT	TATGTATTGTTTATAG	CATTGCTGAATTCAC	TTTATTTATCCTGCA	GTCCACAGACTTGAGA	GCAATAAATGCAAAAC					
1621	1635	1636	1650	1651	1665	1666	1680	1681	1695	1696	1710
v.1	CTAAATGAGAAAATG	GAATCCCTGACAGCT	GTGTCCGTATCAAGC	ATCAGTCTCTCAAAC	AGTTGCCCCAGCCTG	ACAGTGCTAGTCTCT					
v.2	CTAAATGAGAAAATG	GAATCCCTGACAGCT	GTGTCCGTATCAAGC	ATCAGTCTCTCAAAC	AGTTGCCCCAGCCTG	ACAGTGCTAGTCTCT					
v.3	CTAAATGAGAAAATG	GAATCCCTGACAGCT	GTGTCCGTATCAAGC	ATCAGTCTCTCAAAC	AGTTGCCCCAGCCTG	ACAGTGCTAGTCTCT					
1711	1725	1726	1740	1741	1755	1756	1770	1771	1785	1786	1800
v.1	GTTTAAATGGTAAAAG	GAGACTTTGCCATAA	TTTTTCAGATGAAGAT	GTTTCCCAAACACTG	TTTACAGAATGAGAT	GTGACTC-TACAGAT					
v.2	GTTTAAATGGTAAAAG	GAGACTTTGCCATAA	TTTTTCAGATGAAGAT	GTTTCCCAAACACTG	TTTACAGAATGAGAT	GTGACTC-TACAGAT					
v.3	GTTTAAATGGTAAAAG	GAGACTTTGCCATAA	TTTTTCAGATGAAGAT	GTTTCCCAAACACTG	TTTACAGAATGAGAT	GTGACTC-TACAGAT					
1801	1815	1816	1830	1831	1845	1846	1860	1861	1875	1876	1890

v.1	ACCTCATAGAAGACA	ATCCAAGATCATACT	TCATTAACTTGACAG	AGTACGTGTCTTAAA	GGAACATCAAGAAT	TCAATATTTCATT
v.2	ACCTCATAG-----	-----	-----	-----	-----	-----
v.3	ACCTCATAG-----	-----	-----	-----	-----	-----
1891	1905	1906	1920	1921	1935	1936
v.1	AAAAATACTTTTAA	GGCCATTTTATAITA	AGCCAGTGTGGAAA	ACTGAATTTTTTTTA	TTATGTATAATAATC	TCGACACCCAGCTTC
v.2	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----
1981	1995	1996	2010	2011	2025	2026
v.1	TGGAATTGCTGCTTT	CTTTTACAGAAAT	ACTACCCAACAGATT	TCAGGAAGTACTAGT	AGTATCCCAAAGT	GGATAAGCATGTAT
v.2	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----
2071	2085	2086	2100	2101	2115	2116
v.1	TCCTAAGTGTTCAG	AAATGTTTATTICA	CACATAAGTCTTAAT	GTTATTGTTATGATT	AACTTTATAAACAA	CCTTTCCAGATGCT
v.2	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----
2161	2175	2176	2190	2191	2205	2206
v.1	ACAGGGTTTGAATC	TCAAAGTTAACATTT	TTCATTATTGTAAT	CCTAGAACCATAATCT	TTATTATTGTGGTC	ACTGTTATTAAATGA
v.2	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----
2251	2265	2266	2280	2281	2295	2296
v.1	TTTAGGAAATACTTT	CAATATTATTCTGAA	TGGCTGAAGTTAGTC	TAAACTCAAATTAC	TATATGATGATTAA	AACAAATAAAGAG
v.2	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----
2341	2355	2356	2370			
v.1	CGAGGATGGGAAAA	AAAAAAAAAAAAAAA	AAA	2364		
v.2	-----	-----	---	1548		
v.3	-----	-----	---	1557		